



SEQUENCE LISTING

<110> Frances E. Lund
Troy D. Randall
Santiago Partida-Sanchez

<120> CD38 MODULATED CHEMOTAXIS

<130> AP33438 068443.0106

<140> 09/982,616

<141> 2001-10-17

<150> 60/241,065

<151> 2000-10-17

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<210> 1

<211> 1073

<212> DNA

<213> Shistosoma mansoni

<400> 1

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ctctgcacaa	catcaaataa	acttacttag	tgaatatagta	caatcacgat	gtactcagtg	180
gaagggtgaa	catggagcta	ctaataataa	ttgtagtgag	atctggaatt	catttgaaag	240
cattttactt	tcaactcata	ctaaatcagc	atgtgttatg	aatcagggt	tattcgatga	300
ttttgtttat	caattgtttg	aattggaaca	acaacaacaa	cagcgacacc	acacaattca	360
aacggaacaa	tacttccatt	ctcaagtgat	gaacatcatt	cgtggaatgt	gtaaacgtct	420
tggagtatgt	cgttctctag	aaactacatt	tccaggatat	ctgtttgatg	aattgaattg	480
gtgtaatggc	agtttaacag	gcaacacaaa	atacgggact	gtatgtggat	gcgattataa	540
aagtaatggt	gttcatgcgt	tctggcaaag	tgcttcggct	gagtatgcca	ggagagcatc	600
tggtaacatc	tttgtgttac	tgaatggctc	ggccaaagct	ccatttaattg	aaaataaaaac	660
ttttggaaaa	atagaactac	cattgttaaa	acatcctcga	gtacaacaat	taacagtga	720
attagttcat	agtttggaag	atgtaaataa	ccgacaaaca	tgtgaatcgt	ggagtctgca	780
agaacttgca	aacaagctga	actctgtaca	tattcctttt	cgttgcattg	acgatccttt	840
agagttcaga	cattatcaat	gcattgaaaa	tcctggcaaa	caactatgtc	agttttcagc	900
ttcgacgagg	tcaaacgtcg	agacattact	catacttttt	ccgctagtca	tttgtttaac	960
tttttatact	tccatgaatt	gaaataactt	ttcagaacta	aactttgaac	agagaaagag	1020
aacaatgata	ataaaggaat	aggacattaa	tgaaaaaaaa	aaaaaaaaaa	aaa	1073

<210> 2

<211> 353

<212> PRT

<213> Shistosoma mansoni

 $\langle 400 \rangle$ 2[illegible]

<210> 3
<211> 1050
<212> DNA
<213> Artificial Sequence

<220>
<223> SM38 consensus sequence

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ctctgcacaa catcaaataa acttacttag tgaaatagta caatcacgat gtactcagtg 180
gaaggttgaa catggagcta ctaatatag ttgtagttag atctggaatt catttgaaag 240
cattttactt tcaactcata ctaaatacagc atgtgttatg aaatcagggt tattcgatga 300
ttttgtttat caattgtttg aattggaaca acaacaacaa cagcgacacc acacaattca 360
aacggaacaa tacttccatt ctcaagtgtg gaacatcatt cgtggaatgt gtaaacgtct 420
tgagtgatgt cgttctctag aaactacatt tccaggatat ctgtttgatg aattgaattg 480
gtgtaatggc agtttaacag gcaacacaaa atacgggact gtatgtggat gcgattataa 540
aagtaatgtt gttcatgcgt tctggcaaag tgcttcggct gagtatgccg ggagagcatc 600
tggtaacatc tttgtggtac tgaatggctc ggtcaaagct ccatttaattg aaaataaaaac 660
ttttggaaaa atagaactac cattgggttaa aacatcctcg agtacaacaa ttaacagtga 720
aattagttca tagtttgtaa gatgtaaata accgacaaac atgtgaatcg tggagtctgc 780
aagaacttgc aaacaagctg aactctgtac atattccttt tctgttcatt gacgatcctt 840
tagagttcag acattatcaa tgcattgaaa atcctggcaa acaactatgt cagttttcag 900
cttcgacgag gtcaaacgtc gagacattac tcatactttt tccgctagtc atttgtttta 960
ctttttatac ttccatgaat tgaataaact tttcagaact aaactttgaa cagagaaaga 1020
gaacaatgat aataaaggaa taggmcatta 1050

<210> 4
<211> 473
<212> DNA
<213> *Shistosoma mansoni*

<400> 4
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tcgagtacaa caattaacag tgaaattagt tcatagtttg gaagatgtaa ataaccgaca 180
aacatgtgaa tcgtggagtc tgcaagaact tgcaaacaag ctgaactctg tacatattcc 240
ttttcgttgc attgacgac ctttagagtt cagacattat caatgcattg aaaatcctgg 300
caaacaacta tgtcagtttt cagcttcgac gaggtcaaac gtcgagacat tactcatact 360
ttttccgcta gtcatttgtt taacttttta tacttccatg aattgaaata acttttcaga 420
actaaacttt gaacagagaa agagaacaat gataataaag gaataggcca tta 473

<210> 5
<211> 145
<212> DNA
<213> *Shistosoma mansoni*

<400> 5

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aataactttt cagaactaaa ctttg 145

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<210> 6
<211> 280
<212> DNA
<213> Shistosoma mansoni

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<400> 6
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agtaatgttg ttcattgcgtt ctggcaaagt gcttcggctg agtatgccag gagagcatct 180
ggtaacatct ttgtgggtact gaatggctcg gtcaaagctc catttaatga aaataaaact 240
tttgaaaaaa tagaactacc attgggttaa acatcctcga 280

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<210> 7
<211> 1049
<212> DNA
<213> Shistosoma mansoni

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<400> 7
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aattcaaata atgatgaacg taatattggt tcttacttta tcaaataatt ttgtctttta 120
ctctgcacaa catcaaataa acttacttag tgaaatagta caatcācga gtāctcāgtg 180
gaagggtgaa catggagcta ctaatataag ttgtagttag atctggaatt catttgaaag 240
cattttactt tcaactcata ctaaatacagc atgtgttatg aaatcagggg tattcgatga 300
ttttgtttat caattgtttg aattggaaca acaacaacaa cagcgacacc acacaattca 360
aacggaacaa tacttccatt ctcaagtgat gaacatcatt cgtggaatgt gtaaacgtct 420
tggtgatgtg cgttctctag aaactacatt tccaggatat ctgtttgatg aattgaattg 480
gtgtaatggc agtttaacag gcaacacaaa atacgggact gtatgtggat gcgattataa 540
aagtaatggt gttcatgcgt tctggcaaag tgcttcggct gagtatgccg ggagagcatc 600
tggtaacatc tttgtggtac tgaatggctc ggtcaaagct ccatttaatg aaaataaaaac 660
ttttgaaaaa atagaactac cattgttaaa acatcctcga gtacaacaat taacagtga 720
attagttcat agtttggaag atgtaaataa ccgacaaaca tgtgaatcgt ggagtctgca 780
agaacttgca aacaagctga actctgtaca tattcctttt cgttgcattg acgatccttt 840
agagttcaga cattatcaat gcattgaaaa tcctggcaaa caactatgtc agttttcagc 900
ttcgacgagg tcaaacgtcg agacattact catacttttt ccgctagtca tttgtttaac 960
tttttatact tccatgaatt gaaataactt ttcagaacta aactttgaac agagaaagag 1020
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<210> 8
<211> 282
<212> PRT
<213> Aplysia californica

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<400> 8
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Thr Arg Ile Ser Pro Ser Glu Ala Ile Phe Pro Thr Pro Glu Leu Gln

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Asn	Val	Phe	Leu	Gly	Arg	Cys	Lys	Asp	Tyr	Glu	Ile	Thr	Arg	Tyr	Leu	
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Thr	Ile	Leu	Pro	Arg	Val	Lys	Ser	Asp	Cys	Arg	Ala	Leu	Trp	Thr	Asn	
	50					55					60					
Phe	Phe	Lys	Ala	Phe	Ser	Phe	Lys	Ala	Pro	Cys	Asn	Leu	Asp	Leu	Gly	
65					70				75						80	
Ser	Tyr	Lys	Asp	Phe	Phe	Gln	Arg	Ala	Gln	Gln	Thr	Leu	Pro	Lys	Asn	
				85					90					95		
Lys	Val	Met	Phe	Trp	Ser	Gly	Val	Tyr	Asp	Glu	Ala	His	Asp	Phe	Ala	
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Asp	Asp	Gly	Arg	Lys	Tyr	Ile	Thr	Leu	Glu	Asp	Thr	Leu	Pro	Gly	Tyr	
		115					120					125				
Met	Leu	Asn	Ser	Leu	Val	Trp	Cys	Gly	Gln	Arg	Asp	Lys	Pro	Gly	Phe	
	130					135					140					
Asn	Gln	Lys	Val	Cys	Pro	Asp	Phe	Lys	Asp	Cys	Pro	Val	Gln	Ala	Arg	
145					150					155					160	
Glu	Ser	Phe	Trp	Gly	Thr	Ala	Ser	Ser	Ser	Tyr	Ala	His	Ser	Ala	Glu	
				165					170						175	
Gly	Asp	Val	Thr	Tyr	Met	Val	Asp	Gly	Ser	Asn	Pro	Lys	Val	Pro	Ala	
			180					185					190			
Tyr	Arg	Pro	Asp	Ser	Phe	Phe	Gly	Lys	Tyr	Glu	Leu	Pro	Asn	Leu	Thr	
		195					200					205				
Asn	Lys	Val	Thr	Lys	Val	Lys	Val	Ile	Val	Leu	His	Gln	Leu	Gly	Gln	
	210					215					220					
Lys	Ile	Ile	Glu	Arg	Cys	Gly	Ala	Gly	Ser	Leu	Leu	Asp	Leu	Glu	Met	
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				245					250					255		
Ser	Val	Leu	Phe	Leu	Leu	Cys	Ala	Asp	Asn	Pro	Asn	Ala	Arg	Glu	Cys	
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Gln	Leu	Ala	Lys	Arg	Tyr	Tyr	Arg	Ile	Ala							
		275					280									

<210> 9
 <211> 300
 <212> PRT
 <213> Homo sapien

<400> 9
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 Leu Ile Leu Val Val Val Leu Ala Val Val Val Pro Arg Trp Arg Gln
 35 40 45
 Gln Trp Ser Gly Pro Gly Thr Lys Arg Phe Pro Glu Thr Val Leu
 50 55 60
 Ala Arg Cys Val Lys Tyr Thr Glu Ile His Pro Glu Met Arg His Val

65					70					75					80
Asp	Cys	Gln	Ser	Val	Trp	Asp	Ala	Phe	Lys	Gly	Ala	Phe	Ile	Ser	Lys
				85					90					95	
His	Pro	Cys	Asn	Ile	Thr	Glu	Glu	Asp	Tyr	Gln	Pro	Leu	Met	Lys	Leu
			100					105					110		
Gly	Thr	Gln	Thr	Val	Pro	Cys	Asn	Lys	Ile	Leu	Leu	Trp	Ser	Arg	Ile
		115					120					125			
Lys	Asp	Leu	Ala	His	Gln	Phe	Thr	Gln	Val	Gln	Arg	Asp	Met	Phe	Thr
	130					135					140				
Leu	Glu	Asp	Thr	Leu	Leu	Gly	Tyr	Leu	Ala	Asp	Asp	Leu	Thr	Trp	Cys
145					150					155					160
Gly	Glu	Phe	Asn	Thr	Ser	Lys	Ile	Asn	Tyr	Gln	Ser	Cys	Pro	Asp	Trp
			165					170						175	
Arg	Lys	Asp	Cys	Ser	Asn	Asn	Pro	Val	Ser	Val	Phe	Trp	Lys	Thr	Val
			180					185					190		
Ser	Arg	Arg	Phe	Ala	Glu	Ala	Ala	Cys	Asp	Val	Val	His	Val	Met	Leu
		195					200					205			
Asn	Gly	Ser	Arg	Ser	Lys	Ile	Phe	Asp	Lys	Asn	Ser	Thr	Phe	Gly	Ser
	210					215					220				
Val	Glu	Val	His	Asn	Leu	Gln	Pro	Glu	Lys	Val	Gln	Thr	Leu	Glu	Ala
225					230					235					240
Trp	Val	Ile	His	Gly	Gly	Arg	Glu	Asp	Ser	Arg	Asp	Leu	Cys	Gln	Asp
			245					250						255	
Pro	Thr	Ile	Lys	Glu	Leu	Glu	Ser	Ile	Ile	Ser	Lys	Arg	Asn	Ile	Gln
			260					265					270		
Phe	Ser	Cys	Lys	Asn	Ile	Tyr	Arg	Pro	Asp	Lys	Phe	Leu	Gln	Cys	Val
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Lys	Asn	Pro	Glu	Asp	Ser	Ser	Cys	Thr	Ser	Glu	Ile				
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<210> 10

<211> 303

<212> PRT

<213> Shistosoma mansoni

<400> 10

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			20					25					30		
Arg	Cys	Thr	Gln	Trp	Lys	Val	Glu	His	Gly	Ala	Thr	Asn	Ile	Ser	Cys
		35					40					45			
Ser	Glu	Ile	Trp	Asn	Ser	Phe	Glu	Ser	Ile	Leu	Leu	Ser	Thr	His	Thr
	50					55					60				
Lys	Ser	Ala	Cys	Val	Met	Lys	Ser	Gly	Leu	Phe	Asp	Asp	Phe	Val	Tyr
65					70					75					80
Gln	Leu	Phe	Glu	Leu	Glu	Gln	Gln	Gln	Gln	Gln	Arg	His	His	Thr	Ile
			85					90						95	
Gln	Thr	Glu	Gln	Tyr	Phe	His	Ser	Gln	Val	Met	Asn	Ile	Ile	Arg	Gly

			100					105					110				
Met	Cys	Lys	Arg	Leu	Gly	Val	Cys	Arg	Ser	Leu	Glu	Thr	Thr	Phe	Pro		
		115					120					125					
Gly	Tyr	Leu	Phe	Asp	Glu	Leu	Asn	Trp	Cys	Asn	Gly	Ser	Leu	Thr	Gly		
	130					135					140						
Asn	Thr	Lys	Tyr	Gly	Thr	Val	Cys	Gly	Cys	Asp	Tyr	Lys	Ser	Asn	Val		
145					150					155					160		
Val	His	Ala	Phe	Trp	Gln	Ser	Ala	Ser	Ala	Glu	Tyr	Ala	Arg	Arg	Ala		
				165					170					175			
Ser	Gly	Asn	Ile	Phe	Val	Val	Leu	Asn	Gly	Ser	Val	Lys	Ala	Pro	Phe		
			180					185					190				
Asn	Glu	Asn	Lys	Thr	Phe	Gly	Lys	Ile	Glu	Leu	Pro	Leu	Leu	Lys	His		
		195					200					205					
Pro	Arg	Val	Gln	Gln	Leu	Thr	Val	Lys	Leu	Val	His	Ser	Leu	Glu	Asp		
	210					215					220						
Val	Asn	Asn	Arg	Gln	Thr	Cys	Glu	Ser	Trp	Ser	Leu	Gln	Glu	Leu	Ala		
225					230					235					240		
Asn	Lys	Leu	Asn	Ser	Val	His	Ile	Pro	Phe	Arg	Cys	Ile	Asp	Asp	Pro		
				245					250					255			
Leu	Glu	Phe	Arg	His	Tyr	Gln	Cys	Ile	Glu	Asn	Pro	Gly	Lys	Gln	Leu		
			260				265					270					
Cys	Gln	Phe	Ser	Ala	Ser	Thr	Arg	Ser	Asn	Val	Glu	Thr	Leu	Leu	Ile		
		275				280					285						
Leu	Phe	Pro	Leu	Val	Ile	Cys	Leu	Thr	Phe	Tyr	Thr	Ser	Met	Asn			
	290					295					300						

<210> 11

<211> 909

<212> PRT

<213> Artificial Sequence

<220>

<223> Reverse translation of SM38

<400> 11

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			20					25					30				
Asn	Ala	Ala	Tyr	Ala	Thr	His	Thr	Thr	Tyr	Gly	Thr	Asn	Thr	Thr	Tyr		
		35					40					45					
Ala	Ala	Tyr	Trp	Ser	Asn	Gly	Cys	Asn	Cys	Ala	Arg	Cys	Ala	Tyr	Cys		
	50					55					60						
Ala	Arg	Ala	Thr	His	Ala	Ala	Tyr	Tyr	Thr	Asn	Tyr	Thr	Asn	Trp	Ser		
65					70					75					80		
Asn	Gly	Ala	Arg	Ala	Thr	His	Gly	Thr	Asn	Cys	Ala	Arg	Trp	Ser	Asn		
			85					90						95			
Met	Gly	Asn	Thr	Gly	Tyr	Ala	Cys	Asn	Cys	Ala	Arg	Thr	Gly	Gly	Ala		
			100					105					110				

Ala	Arg	Gly	Thr	Asn	Gly	Ala	Arg	Cys	Ala	Tyr	Gly	Gly	Asn	Gly	Cys	
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Asn	Ala	Cys	Asn	Ala	Ala	Tyr	Ala	Thr	His	Trp	Ser	Asn	Thr	Gly	Tyr	
	130					135					140					
Trp	Ser	Asn	Gly	Ala	Arg	Ala	Thr	His	Thr	Gly	Gly	Ala	Ala	Tyr	Trp	
145					150					155					160	
Ser	Asn	Thr	Thr	Tyr	Gly	Ala	Arg	Trp	Ser	Asn	Ala	Thr	His	Tyr	Thr	
			165					170						175		
Asn	Tyr	Thr	Asn	Trp	Ser	Asn	Ala	Cys	Asn	Cys	Ala	Tyr	Ala	Cys	Asn	
			180					185					190			
Ala	Ala	Arg	Trp	Ser	Asn	Gly	Cys	Asn	Thr	Gly	Tyr	Gly	Thr	Asn	Ala	
		195					200					205				
Thr	Gly	Ala	Ala	Arg	Trp	Ser	Asn	Gly	Gly	Asn	Tyr	Thr	Asn	Thr	Thr	
	210					215					220					
Tyr	Gly	Ala	Tyr	Gly	Ala	Tyr	Thr	Thr	Tyr	Gly	Thr	Asn	Thr	Ala	Tyr	
225					230					235					240	
Cys	Ala	Arg	Tyr	Thr	Asn	Thr	Thr	Tyr	Gly	Ala	Arg	Tyr	Thr	Asn	Gly	
			245						250					255		
Ala	Arg	Cys	Ala	Arg	Cys	Ala	Arg	Cys	Ala	Arg	Cys	Ala	Arg	Cys	Ala	
		260						265					270			
Arg	Met	Gly	Asn	Cys	Ala	Tyr	Cys	Ala	Tyr	Ala	Cys	Asn	Ala	Thr	His	
	275						280					285				
Cys	Ala	Arg	Ala	Cys	Asn	Gly	Ala	Arg	Cys	Ala	Arg	Thr	Ala	Tyr	Thr	
	290					295					300					
Thr	Tyr	Cys	Ala	Tyr	Trp	Ser	Asn	Cys	Ala	Arg	Gly	Thr	Asn	Ala	Thr	
305					310					315					320	
Gly	Ala	Ala	Tyr	Ala	Thr	His	Ala	Thr	His	Met	Gly	Asn	Gly	Gly	Asn	
			325						330					335		
Ala	Thr	Gly	Thr	Gly	Tyr	Ala	Ala	Arg	Met	Gly	Asn	Tyr	Thr	Asn	Gly	
			340					345						350		
Gly	Asn	Gly	Thr	Asn	Thr	Gly	Tyr	Met	Gly	Asn	Trp	Ser	Asn	Tyr	Thr	
	355					360						365				
Asn	Gly	Ala	Arg	Ala	Cys	Asn	Ala	Cys	Asn	Thr	Thr	Tyr	Cys	Cys	Asn	
	370					375					380					
Gly	Gly	Asn	Thr	Ala	Tyr	Tyr	Thr	Asn	Thr	Thr	Tyr	Gly	Ala	Tyr	Gly	
385					390					395					400	
Ala	Arg	Tyr	Thr	Asn	Ala	Ala	Tyr	Thr	Gly	Gly	Thr	Gly	Tyr	Ala	Ala	
			405						410					415		
Tyr	Gly	Gly	Asn	Trp	Ser	Asn	Tyr	Thr	Asn	Ala	Cys	Asn	Gly	Gly	Asn	
			420					425					430			
Ala	Ala	Tyr	Ala	Cys	Asn	Ala	Ala	Arg	Thr	Ala	Tyr	Gly	Gly	Asn	Ala	
	435						440					445				
Cys	Asn	Gly	Thr	Asn	Thr	Gly	Tyr	Gly	Gly	Asn	Thr	Gly	Tyr	Gly	Ala	
	450					455					460					
Tyr	Thr	Ala	Tyr	Ala	Ala	Arg	Trp	Ser	Asn	Ala	Ala	Tyr	Gly	Thr	Asn	
465					470					475					480	
Gly	Thr	Asn	Cys	Ala	Tyr	Gly	Cys	Asn	Thr	Thr	Tyr	Thr	Gly	Gly	Cys	
			485						490					495		
Ala	Arg	Trp	Ser	Asn	Gly	Cys	Asn	Trp	Ser	Asn	Gly	Cys	Asn	Gly	Ala	
			500					505					510			

Arg	Thr	Ala	Tyr	Gly	Cys	Asn	Met	Gly	Asn	Met	Gly	Asn	Gly	Cys	Asn
		515					520						525		
Trp	Ser	Asn	Gly	Gly	Asn	Ala	Ala	Tyr	Ala	Thr	His	Thr	Thr	Tyr	Gly
	530					535					540				
Thr	Asn	Gly	Thr	Asn	Tyr	Thr	Asn	Ala	Ala	Tyr	Gly	Gly	Asn	Trp	Ser
545					550					555					560
Asn	Gly	Thr	Asn	Ala	Ala	Arg	Gly	Cys	Asn	Cys	Cys	Asn	Thr	Thr	Tyr
				565					570					575	
Ala	Ala	Tyr	Gly	Ala	Arg	Ala	Ala	Tyr	Ala	Ala	Arg	Ala	Cys	Asn	Thr
			580					585					590		
Thr	Tyr	Gly	Gly	Asn	Ala	Ala	Arg	Ala	Thr	His	Gly	Ala	Arg	Tyr	Thr
		595					600					605			
Asn	Cys	Cys	Asn	Tyr	Thr	Asn	Tyr	Thr	Asn	Ala	Ala	Arg	Cys	Ala	Tyr
	610					615					620				
Cys	Cys	Asn	Met	Gly	Asn	Gly	Thr	Asn	Cys	Ala	Arg	Cys	Ala	Arg	Tyr
625					630					635					640
Thr	Asn	Ala	Cys	Asn	Gly	Thr	Asn	Ala	Ala	Arg	Tyr	Thr	Asn	Gly	Thr
				645					650					655	
Asn	Cys	Ala	Tyr	Trp	Ser	Asn	Tyr	Thr	Asn	Gly	Ala	Arg	Gly	Ala	Tyr
			660					665					670		
Gly	Thr	Asn	Ala	Ala	Tyr	Ala	Ala	Tyr	Met	Gly	Asn	Cys	Ala	Arg	Ala
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		755					760					765			
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Tyr	Cys	Cys	Asn	Gly	Gly	Asn	Ala	Ala	Arg	Cys	Ala	Arg	Tyr	Thr	Asn
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			820					825					830		
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